

**AMENDMENT**

**IN THE SPECIFICATION.**

Please **delete** the amended first paragraph of the specification and substitute therefor the following **new** paragraph:

This application is a continuation of U.S. patent application Serial No. 09/189,103, filed November 9, 1998, which is a continuation of U.S. patent application Serial No. 08/650,400, filed May 20, 1996, now U.S. Patent No. 5,837,458, which is a continuation-in-part of U.S. patent application Serial No. 08/621,430, filed March 25, 1996, (abandoned), and of U.S. patent application Serial No. 08/621,859, filed March 25, 1996, now U.S. Patent No. 6,117,679, and of U.S. patent application Serial No. 08/537,874, filed March 4, 1996, now U.S. Patent No. 5,830,721 (U.S. National Phase of PCT/US95/02126, filed February 17, 1995), and of U.S. patent application Serial No. 08/198,431, filed February 17, 1994, now U.S. Patent No. 5,605,793, the specifications of which are incorporated herein by reference in their entirety for all purposes.

In accordance with 37 CFR §1.121 a marked up version of the above-amended paragraph illustrating the changes introduced by the amendment is provided in Appendix A.

**IN THE CLAIMS:**

Please **cancel** claim 83.

Please **amend** the claims by substituting the following claims for the corresponding previously pending claims of the same numbers:

**31. (Amended)** A method for combinatorial cassette-based recombination, comprising: conjoining a plurality of homologous recombination sites to a plurality of subsequences of at least one nucleic acid, thereby producing a plurality of recombination cassettes; recombining the recombination cassettes, or fragments thereof, at the recombination sites, thereby producing a plurality of permutations of the recombination cassettes within a plurality of resulting recombinant nucleic acids; and, selecting the plurality of recombinant nucleic acids for one or more property or encoded activity.

**33. (Amended)** A method for permuting subsequences of interest in at least one nucleic acid, the method comprising: identifying functionally similar subsequences in the at least one nucleic acid;